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Sequence Listing was accepted.

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217-9197 (toll free).

Reviewer: Saleem, Syed (ASRC)

Timestamp: [year=2010; month=7; day=28; hr=11; min=0; sec=30; ms=525;]

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Application No: 10522341 Version No: 3.0

Input Set:**Output Set:**

Started: 2010-07-22 15:40:42.953
Finished: 2010-07-22 15:40:50.330
Elapsed: 0 hr(s) 0 min(s) 7 sec(s) 377 ms
Total Warnings: 126
Total Errors: 0
No. of SeqIDs Defined: 179
Actual SeqID Count: 179

| Error code | Error Description |
|------------|---|
| W 213 | Artificial or Unknown found in <213> in SEQ ID (3) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (4) |
| W 402 | Undefined organism found in <213> in SEQ ID (13) |
| W 402 | Undefined organism found in <213> in SEQ ID (14) |
| W 402 | Undefined organism found in <213> in SEQ ID (15) |
| W 402 | Undefined organism found in <213> in SEQ ID (16) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (49) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (50) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (51) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (52) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (53) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (54) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (55) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (56) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (57) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (58) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (69) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (70) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (71) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (72) |

Input Set:

Output Set:

Started: 2010-07-22 15:40:42.953
Finished: 2010-07-22 15:40:50.330
Elapsed: 0 hr(s) 0 min(s) 7 sec(s) 377 ms
Total Warnings: 126
Total Errors: 0
No. of SeqIDs Defined: 179
Actual SeqID Count: 179

| Error code | Error Description |
|------------|--|
| W 213 | Artificial or Unknown found in <213> in SEQ ID (73) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (74) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (75) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (76) This error has occurred more than 20 times, will not be displayed |

<210> 1
 <211> 1284
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)..(1281)
 <223> coding for cytosine deaminase (codA)

<400> 1
 gtg tcg aat aac gct tta caa aca att att aac gcc cgg tta cca ggc 48
 Val Ser Asn Asn Ala Leu Gln Thr Ile Ile Asn Ala Arg Leu Pro Gly
 1 5 10 15
 gaa gag ggg ctg tgg cag att cat ctg cag gac gga aaa atc agc gcc 96
 Glu Glu Gly Leu Trp Gln Ile His Leu Gln Asp Gly Lys Ile Ser Ala
 20 25 30
 att gat gcg caa tcc ggc gtg atg ccc ata act gaa aac agc ctg gat 144
 Ile Asp Ala Gln Ser Gly Val Met Pro Ile Thr Glu Asn Ser Leu Asp
 35 40 45
 gcc gaa caa ggt tta gtt ata ccg ccg ttt gtg gag cca cat att cac 192
 Ala Glu Gln Gly Leu Val Ile Pro Pro Phe Val Glu Pro His Ile His
 50 55 60
 ctg gac acc acg caa acc gcc gga caa ccg aac tgg aat cag tcc ggc 240
 Leu Asp Thr Thr Gln Thr Ala Gly Gln Pro Asn Trp Asn Gln Ser Gly
 65 70 75 80
 acg ctg ttt gaa ggc att gaa cgc tgg gcc gag cgc aaa gcg tta tta 288
 Thr Leu Phe Glu Gly Ile Glu Arg Trp Ala Glu Arg Lys Ala Leu Leu
 85 90 95
 acc cat gac gat gtg aaa caa cgc gca tgg caa acg ctg aaa tgg cag 336
 Thr His Asp Asp Val Lys Gln Arg Ala Trp Gln Thr Leu Lys Trp Gln
 100 105 110
 att gcc aac ggc att cag cat gtg cgt acc cat gtc gat gtt tcg gat 384
 Ile Ala Asn Gly Ile Gln His Val Arg Thr His Val Asp Val Ser Asp
 115 120 125
 gca acg cta act gcg ctg aaa gca atg ctg gaa gtg aag cag gaa gtc 432
 Ala Thr Leu Thr Ala Leu Lys Ala Met Leu Glu Val Lys Gln Glu Val
 130 135 140
 gcg ccg tgg att gat ctg caa atc gtc gcc ttc cct cag gaa ggg att 480
 Ala Pro Trp Ile Asp Leu Gln Ile Val Ala Phe Pro Gln Glu Gly Ile
 145 150 155 160
 ttg tcg tat ccc aac ggt gaa gcg ttg ctg gaa gag gcg tta cgc tta 528
 Leu Ser Tyr Pro Asn Gly Glu Ala Leu Leu Glu Glu Ala Leu Arg Leu
 165 170 175
 ggg gca gat gta gtg ggg gcg att ccg cat ttt gaa ttt acc cgt gaa 576
 Gly Ala Asp Val Val Gly Ala Ile Pro His Phe Glu Phe Thr Arg Glu
 180 185 190
 tac ggc gtg gag tcg ctg cat aaa acc ttc gcc ctg gcg caa aaa tac 624
 Tyr Gly Val Glu Ser Leu His Lys Thr Phe Ala Leu Ala Gln Lys Tyr
 195 200 205
 gac cgt ctc atc gac gtt cac tgt gat gag atc gat gac gag cag tcg 672
 Asp Arg Leu Ile Asp Val His Cys Asp Glu Ile Asp Asp Glu Gln Ser
 210 215 220
 cgc ttt gtc gaa acc gtt gct gcc ctg gcg cac cat gaa ggc atg ggc 720
 Arg Phe Val Glu Thr Val Ala Ala Leu Ala His His Glu Gly Met Gly
 225 230 235 240
 gcg cga gtc acc gcc agc cac acc acg gca atg cac tcc tat aac ggg 768

| | | | | |
|---|---------------------|---------------------|---------|--|
| Ala Arg Val Thr | Ala Ser His Thr Thr | Ala Met His Ser Tyr | Asn Gly | |
| 245 | 250 | 255 | | |
| gcg tat acc tca cgc ctg ttc cgc ttg ctg aaa atg tcc ggt att aac | 816 | | | |
| Ala Tyr Thr Ser Arg Leu Phe Arg Leu Leu Lys Met Ser Gly Ile Asn | | | | |
| 260 | 265 | 270 | | |
| ttt gtc gcc aac ccg ctg gtc aat att cat ctg caa gga cgt ttc gat | 864 | | | |
| Phe Val Ala Asn Pro Leu Val Asn Ile His Leu Gln Gly Arg Phe Asp | | | | |
| 275 | 280 | 285 | | |
| acg tat cca aaa cgt cgc ggc atc acg cgc gtt aaa gag atg ctg gag | 912 | | | |
| Thr Tyr Pro Lys Arg Arg Gly Ile Thr Arg Val Lys Glu Met Leu Glu | | | | |
| 290 | 295 | 300 | | |
| tcc ggc att aac gtc tgc ttt ggt cac gat gat gtc ttc gat ccg tgg | 960 | | | |
| Ser Gly Ile Asn Val Cys Phe Gly His Asp Asp Val Phe Asp Pro Trp | | | | |
| 305 | 310 | 315 | 320 | |
| tat ccg ctg gga acg gcg aat atg ctg caa gtg ctg cat atg ggg ctg | 1008 | | | |
| Tyr Pro Leu Gly Thr Ala Asn Met Leu Gln Val Leu His Met Gly Leu | | | | |
| 325 | 330 | 335 | | |
| cat gtt tgc cag ttg atg ggc tac ggg cag att aac gat ggc ctg aat | 1056 | | | |
| His Val Cys Gln Leu Met Gly Tyr Gly Gln Ile Asn Asp Gly Leu Asn | | | | |
| 340 | 345 | 350 | | |
| tta atc acc cac cac agc gca agg acg ttg aat ttg cag gat tac ggc | 1104 | | | |
| Leu Ile Thr His His Ser Ala Arg Thr Leu Asn Leu Gln Asp Tyr Gly | | | | |
| 355 | 360 | 365 | | |
| att gcc gcc gga aac agc gcc aac ctg att atc ctg ccg gct gaa aat | 1152 | | | |
| Ile Ala Ala Gly Asn Ser Ala Asn Leu Ile Ile Leu Pro Ala Glu Asn | | | | |
| 370 | 375 | 380 | | |
| ggg ttt gat gcg ctg cgc cgt cag gtt ccg gta cgt tat tcg gta cgt | 1200 | | | |
| Gly Phe Asp Ala Leu Arg Arg Gln Val Pro Val Arg Tyr Ser Val Arg | | | | |
| 385 | 390 | 395 | 400 | |
| ggc ggc aag gtg att gcc agc aca caa ccg gca caa acc acc gta tat | 1248 | | | |
| Gly Gly Lys Val Ile Ala Ser Thr Gln Pro Ala Gln Thr Thr Val Tyr | | | | |
| 405 | 410 | 415 | | |
| ctg gag cag cca gaa gcc atc gat tac aaa cgt tga | 1284 | | | |
| Leu Glu Gln Pro Glu Ala Ile Asp Tyr Lys Arg | | | | |
| 420 | 425 | | | |

<210> 2

<211> 427

<212> PRT

<213> Escherichia coli

<400> 2

| | |
|---|-----|
| Val Ser Asn Asn Ala Leu Gln Thr Ile Ile Asn Ala Arg Leu Pro Gly | |
| 1 | 15 |
| Glu Glu Gly Leu Trp Gln Ile His Leu Gln Asp Gly Lys Ile Ser Ala | |
| 20 | 30 |
| Ile Asp Ala Gln Ser Gly Val Met Pro Ile Thr Glu Asn Ser Leu Asp | |
| 35 | 45 |
| Ala Glu Gln Gly Leu Val Ile Pro Pro Phe Val Glu Pro His Ile His | |
| 50 | 60 |
| Leu Asp Thr Thr Gln Thr Ala Gly Gln Pro Asn Trp Asn Gln Ser Gly | |
| 65 | 80 |
| Thr Leu Phe Glu Gly Ile Glu Arg Trp Ala Glu Arg Lys Ala Leu Leu | |
| 85 | 95 |
| Thr His Asp Asp Val Lys Gln Arg Ala Trp Gln Thr Leu Lys Trp Gln | |
| 100 | 110 |

| | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ile | Ala | Asn | Gly | Ile | Gln | His | Val | Arg | Thr | His | Val | Asp | Val | Ser | Asp | 115 | 120 | 125 |
| Ala | Thr | Leu | Thr | Ala | Leu | Lys | Ala | Met | Leu | Glu | Val | Lys | Gln | Glu | Val | 130 | 135 | 140 |
| Ala | Pro | Trp | Ile | Asp | Leu | Gln | Ile | Val | Ala | Phe | Pro | Gln | Glu | Gly | Ile | 145 | 150 | 155 |
| Leu | Ser | Tyr | Pro | Asn | Gly | Glu | Ala | Leu | Leu | Glu | Glu | Ala | Leu | Arg | Leu | 165 | 170 | 175 |
| Gly | Ala | Asp | Val | Val | Gly | Ala | Ile | Pro | His | Phe | Glu | Phe | Thr | Arg | Glu | 180 | 185 | 190 |
| Tyr | Gly | Val | Glu | Ser | Leu | His | Lys | Thr | Phe | Ala | Leu | Ala | Gln | Lys | Tyr | 195 | 200 | 205 |
| Asp | Arg | Leu | Ile | Asp | Val | His | Cys | Asp | Glu | Ile | Asp | Asp | Glu | Gln | Ser | 210 | 215 | 220 |
| Arg | Phe | Val | Glu | Thr | Val | Ala | Ala | Leu | Ala | His | His | Glu | Gly | Met | Gly | 225 | 230 | 235 |
| Ala | Arg | Val | Thr | Ala | Ser | His | Thr | Thr | Ala | Met | His | Ser | Tyr | Asn | Gly | 245 | 250 | 255 |
| Ala | Tyr | Thr | Ser | Arg | Leu | Phe | Arg | Leu | Leu | Lys | Met | Ser | Gly | Ile | Asn | 260 | 265 | 270 |
| Phe | Val | Ala | Asn | Pro | Leu | Val | Asn | Ile | His | Leu | Gln | Gly | Arg | Phe | Asp | 275 | 280 | 285 |
| Thr | Tyr | Pro | Lys | Arg | Arg | Gly | Ile | Thr | Arg | Val | Lys | Glu | Met | Leu | Glu | 290 | 295 | 300 |
| Ser | Gly | Ile | Asn | Val | Cys | Phe | Gly | His | Asp | Asp | Val | Phe | Asp | Pro | Trp | 305 | 310 | 315 |
| Tyr | Pro | Leu | Gly | Thr | Ala | Asn | Met | Leu | Gln | Val | Leu | His | Met | Gly | Leu | 325 | 330 | 335 |
| His | Val | Cys | Gln | Leu | Met | Gly | Tyr | Gly | Gln | Ile | Asn | Asp | Gly | Leu | Asn | 340 | 345 | 350 |
| Leu | Ile | Thr | His | His | Ser | Ala | Arg | Thr | Leu | Asn | Leu | Gln | Asp | Tyr | Gly | 355 | 360 | 365 |
| Ile | Ala | Ala | Gly | Asn | Ser | Ala | Asn | Leu | Ile | Ile | Leu | Pro | Ala | Glu | Asn | 370 | 375 | 380 |
| Gly | Phe | Asp | Ala | Leu | Arg | Arg | Gln | Val | Pro | Val | Arg | Tyr | Ser | Val | Arg | 385 | 390 | 395 |
| Gly | Gly | Lys | Val | Ile | Ala | Ser | Thr | Gln | Pro | Ala | Gln | Thr | Thr | Val | Tyr | 405 | 410 | 415 |
| Leu | Glu | Gln | Pro | Glu | Ala | Ile | Asp | Tyr | Lys | Arg | | | | | | 420 | 425 | |

<210> 3

<211> 1284

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence: coding for
cytosine deaminase (codA)

<220>

<221> misc_feature

<222> (1)..(3)

<223> mutation of GTG to ATG start codon for expression
in eukaryotic hosts

<220>

<221> CDS

<222> (1)..(1281)

<223> coding for cytosine deaminase (codA)

<400> 3

| | |
|---|-----|
| atg tcg aat aac gct tta caa aca att att aac gcc cgg tta cca ggc | 48 |
| Met Ser Asn Asn Ala Leu Gln Thr Ile Ile Asn Ala Arg Leu Pro Gly | |
| 1 5 10 15 | |
| gaa gag ggg ctg tgg cag att cat ctg cag gac gga aaa atc agc gcc | 96 |
| Glu Glu Gly Leu Trp Gln Ile His Leu Gln Asp Gly Lys Ile Ser Ala | |
| 20 25 30 | |
| att gat gcg caa tcc ggc gtg atg ccc ata act gaa aac agc ctg gat | 144 |
| Ile Asp Ala Gln Ser Gly Val Met Pro Ile Thr Glu Asn Ser Leu Asp | |
| 35 40 45 | |
| gcc gaa caa ggt tta gtt ata ccg ccg ttt gtg gag cca cat att cac | 192 |
| Ala Glu Gln Gly Leu Val Ile Pro Pro Phe Val Glu Pro His Ile His | |
| 50 55 60 | |
| ctg gac acc acg caa acc gcc gga caa ccg aac tgg aat cag tcc ggc | 240 |
| Leu Asp Thr Thr Gln Thr Ala Gly Gln Pro Asn Trp Asn Gln Ser Gly | |
| 65 70 75 80 | |
| acg ctg ttt gaa ggc att gaa cgc tgg gcc gag cgc aaa gcg tta tta | 288 |
| Thr Leu Phe Glu Gly Ile Glu Arg Trp Ala Glu Arg Lys Ala Leu Leu | |
| 85 90 95 | |
| acc cat gac gat gtg aaa caa cgc gca tgg caa acg ctg aaa tgg cag | 336 |
| Thr His Asp Asp Val Lys Gln Arg Ala Trp Gln Thr Leu Lys Trp Gln | |
| 100 105 110 | |
| att gcc aac ggc att cag cat gtg cgt acc cat gtc gat gtt tcg gat | 384 |
| Ile Ala Asn Gly Ile Gln His Val Arg Thr His Val Asp Val Ser Asp | |
| 115 120 125 | |
| gca acg cta act gcg ctg aaa gca atg ctg gaa gtg aag cag gaa gtc | 432 |
| Ala Thr Leu Thr Ala Leu Lys Ala Met Leu Glu Val Lys Gln Glu Val | |
| 130 135 140 | |
| gcg ccg tgg att gat ctg caa atc gtc gcc ttc cct cag gaa ggg att | 480 |
| Ala Pro Trp Ile Asp Leu Gln Ile Val Ala Phe Pro Gln Glu Gly Ile | |
| 145 150 155 160 | |
| ttg tcg tat ccc aac ggt gaa gcg ttg ctg gaa gag gcg tta cgc tta | 528 |
| Leu Ser Tyr Pro Asn Gly Glu Ala Leu Leu Glu Glu Ala Leu Arg Leu | |
| 165 170 175 | |
| ggg gca gat gta gtg ggg gcg att ccg cat ttt gaa ttt acc cgt gaa | 576 |
| Gly Ala Asp Val Val Gly Ala Ile Pro His Phe Glu Phe Thr Arg Glu | |
| 180 185 190 | |
| tac ggc gtg gag tcg ctg cat aaa acc ttc gcc ctg gcg caa aaa tac | 624 |
| Tyr Gly Val Glu Ser Leu His Lys Thr Phe Ala Leu Ala Gln Lys Tyr | |
| 195 200 205 | |
| gac cgt ctc atc gac gtt cac tgt gat gag atc gat gac gag cag tcg | 672 |
| Asp Arg Leu Ile Asp Val His Cys Asp Glu Ile Asp Asp Glu Gln Ser | |
| 210 215 220 | |
| cgc ttt gtc gaa acc gtt gct gcc ctg gcg cac cat gaa ggc atg ggc | 720 |
| Arg Phe Val Glu Thr Val Ala Ala Leu Ala His His Glu Gly Met Gly | |
| 225 230 235 240 | |
| gcg cga gtc acc gcc agc cac acc acg gca atg cac tcc tat aac ggg | 768 |
| Ala Arg Val Thr Ala Ser His Thr Thr Ala Met His Ser Tyr Asn Gly | |
| 245 250 255 | |
| gcg tat acc tca cgc ctg ttc cgc ttg ctg aaa atg tcc ggt att aac | 816 |
| Ala Tyr Thr Ser Arg Leu Phe Arg Leu Leu Lys Met Ser Gly Ile Asn | |
| 260 265 270 | |

```

ttt gtc gcc aac ccg ctg gtc aat att cat ctg caa gga cgt ttc gat      864
Phe Val Ala Asn Pro Leu Val Asn Ile His Leu Gln Gly Arg Phe Asp
      275                      280                      285

acg tat cca aaa cgt cgc ggc atc acg cgc gtt aaa gag atg ctg gag      912
Thr Tyr Pro Lys Arg Arg Gly Ile Thr Arg Val Lys Glu Met Leu Glu
      290                      295                      300

tcc ggc att aac gtc tgc ttt ggt cac gat gat gtc ttc gat ccg tgg      960
Ser Gly Ile Asn Val Cys Phe Gly His Asp Asp Val Phe Asp Pro Trp
      305                      310                      315                      320

tat ccg ctg gga acg gcg aat atg ctg caa gtg ctg cat atg ggg ctg      1008
Tyr Pro Leu Gly Thr Ala Asn Met Leu Gln Val Leu His Met Gly Leu
      325                      330                      335

cat gtt tgc cag ttg atg ggc tac ggg cag att aac gat ggc ctg aat      1056
His Val Cys Gln Leu Met Gly Tyr Gly Gln Ile Asn Asp Gly Leu Asn
      340                      345                      350

tta atc acc cac cac agc gca agg acg ttg aat ttg cag gat tac ggc      1104
Leu Ile Thr His His Ser Ala Arg Thr Leu Asn Leu Gln Asp Tyr Gly
      355                      360                      365

att gcc gcc gga aac agc gcc aac ctg att atc ctg ccg gct gaa aat      1152
Ile Ala Ala Gly Asn Ser Ala Asn Leu Ile Ile Leu Pro Ala Glu Asn
      370                      375                      380

ggg ttt gat gcg ctg cgc cgt cag gtt ccg gta cgt tat tcg gta cgt      1200
Gly Phe Asp Ala Leu Arg Arg Gln Val Pro Val Arg Tyr Ser Val Arg
      385                      390                      395                      400

ggc ggc aag gtg att gcc agc aca caa ccg gca caa acc acc gta tat      1248
Gly Gly Lys Val Ile Ala Ser Thr Gln Pro Ala Gln Thr Thr Val Tyr
      405                      410                      415

ctg gag cag cca gaa gcc atc gat tac aaa cgt tga      1284
Leu Glu Gln Pro Glu Ala Ile Asp Tyr Lys Arg
      420                      425

```

<210> 4

<211> 427

<212> PRT

<213> Artificial sequence

<220>

<223> Description of the artificial sequence: coding for
cytosine deaminase (codA)

<400> 4

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Met Ser Asn Asn Ala Leu Gln Thr Ile Ile Asn Ala Arg Leu Pro Gly
  1                      5                      10                      15
Glu Glu Gly Leu Trp Gln Ile His Leu Gln Asp Gly Lys Ile Ser Ala
      20                      25                      30
Ile Asp Ala Gln Ser Gly Val Met Pro Ile Thr Glu Asn Ser Leu Asp
      35                      40                      45
Ala Glu Gln Gly Leu Val Ile Pro Pro Phe Val Glu Pro His Ile His
      50                      55                      60
Leu Asp Thr Thr Gln Thr Ala Gly Gln Pro Asn Trp Asn Gln Ser Gly
      65                      70                      75                      80
Thr Leu Phe Glu Gly Ile Glu Arg Trp Ala Glu Arg Lys Ala Leu Leu
      85                      90                      95
Thr His Asp Asp Val Lys Gln Arg Ala Trp Gln Thr Leu Lys Trp Gln
      100                      105                      110
Ile Ala Asn Gly Ile Gln His Val Arg Thr His Val Asp Val Ser Asp

```


| | | | | |
|---|-----|-----|-----|-----|
| 115 | | 120 | | 125 |
| Ala Thr Leu Thr Ala Leu Lys Ala Met Leu Glu Val Lys Gln Glu Val | | | | |
| 130 | | 135 | | 140 |
| Ala Pro Trp Ile Asp Leu Gln Ile Val Ala Phe Pro Gln Glu Gly Ile | | | | |
| 145 | | 150 | | 155 |
| Leu Ser Tyr Pro Asn Gly Glu Ala Leu Leu Glu Glu Ala Leu Arg Leu | | | | |
| | 165 | | 170 | 175 |
| Gly Ala Asp Val Val Gly Ala Ile Pro His Phe Glu Phe Thr Arg Glu | | | | |
| | 180 | | 185 | 190 |
| Tyr Gly Val Glu Ser Leu His Lys Thr Phe Ala Leu Ala Gln Lys Tyr | | | | |
| | 195 | | 200 | 205 |
| Asp Arg Leu Ile Asp Val His Cys Asp Glu Ile Asp Asp Glu Gln Ser | | | | |
| | 210 | | 215 | 220 |
| Arg Phe Val Glu Thr Val Ala Ala Leu Ala His His Glu Gly Met Gly | | | | |
| 225 | | 230 | | 235 |
| Ala Arg Val Thr Ala Ser His Thr Thr Ala Met His Ser Tyr Asn Gly | | | | |